

1709

OIPE

RAW SEQUENCE LISTING

DATE: 11/01/2001

PATENT APPLICATION: US/09/981,318

TIME: 13:54:04

Input Set : A:\LEX-0255-USA SEQLIST.txt

Output Set: N:\CRF3\11012001\I981318.raw

ENTERED

4 <110> APPLICANT: Walke, D. Wade
 5 Scoville, John
 7 <120> TITLE OF INVENTION: Novel Human Semaphorin Proteins and Polynucleotides Encoding
 the Same

9 <130> FILE REFERENCE: LEX-0255-USA

C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/981,318

C--> 11 <141> CURRENT FILING DATE: 2001-10-17

11 <150> PRIOR APPLICATION NUMBER: US 60/241,194

12 <151> PRIOR FILING DATE: 2000-10-17

14 <160> NUMBER OF SEQ ID NOS: 35

16 <170> SOFTWARE: FastSEQ for Windows Version 4.0

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19 <211> LENGTH: 2304

20 <212> TYPE: DNA

21 <213> ORGANISM: homo sapiens

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26	gagcccagc	cgcgggacac	cgctcgtcct	gctctccgaa	tgctgcgcac	cgcgatgggc	180
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30	tccaactaca	cagcccttct	gctgagcagg	gatggcagga	ccctgtacgt	gggtgctcga	420
31	gaggccctct	ttgcactcag	tagcaacctc	agcttcctgc	caggcgggga	gtaccaggag	480
32	ctgctttggg	gtgcagacgc	agagaagaaa	cagcagtgc	gcttcaagg	caaggacca	540
33	cagcgcgact	gtcaaaacta	catcaagatc	ctcctgcgc	tcagcggcag	tcacctgttc	600
34	acctgtggca	cagcagcctt	cagccccatg	tgtacctaca	tcaacatgga	gaacttcacc	660
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37	agcagcttcc	aagggaatga	cccggccatc	tcgcggagcc	aaagccttcg	ccccaccaag	840
38	accgagagct	ccctcaactg	gctgcaagac	ccagcttttg	tggcctcagc	ctacattcct	900
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40	ggccaggaat	ttgagttctt	tgagaacacc	attgtgtccc	gcattgccc	catctgcaag	1020
41	ggcgatgagg	gtggagagcg	ggtgctacag	cagcgtgga	cctccttctt	caaggcccag	1080
42	ctgctgtgct	cacggcccga	cgatggcttc	cccttcaacg	tgctgcagga	tgtcttcacg	1140
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47	aagatcaact	catccctgca	gctcccagac	cgcgtgctga	acttctctca	ggaccatttc	1440
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49	cgcgtggctg	tacaccgcgt	ccctggcctg	caccacacct	acgatgtcct	cttctgggc	1560
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51	gagctgcaga	tcttctcatc	gggacagccc	gtgcagaatc	tgctcctgga	caccacag	1680
52	gggctgctgt	atgcggcctc	acactcgggc	gtagtccagg	tgcccagggc	caactgcagc	1740
53	ctgtacagga	gctgtgggga	ctgcctcctc	gcccgggacc	cctaactgtgc	ttggagcggc	1800
54	tccagctgca	agcagctcag	cctctaccag	cctcagctgg	ccaccaggcc	gtggatccag	1860
55	gacatcgagg	gagccagcgc	caaggacctt	tgacgcgcgt	cttcgggtgt	gtccccgtct	1920

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58 cccgtcaatg cctcggcctc ctgccacgtg ctaccactg gggacctgct gctggtgggc 2100
59 acccaacagc tgggggagtt ccagtgtctg tccactagagg agggcttcca gcagctggta 2160
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75 35 40 45
76 Ala Pro Ala Leu Arg Met Leu Arg Thr Ala Met Gly Leu Arg Ser Trp
77 50 55 60
78 Leu Ala Ala Pro Trp Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu
79 65 70 75 80
80 Leu Leu Leu Leu Leu Leu Leu Gln Pro Pro Pro Thr Trp Ala
81 85 90 95
82 Leu Ser Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe
83 100 105 110
84 Leu Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu
85 115 120 125
86 Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu Phe
87 130 135 140
88 Ala Leu Ser Ser Asn Leu Ser Phe Leu Pro Gly Gly Glu Tyr Gln Glu
89 145 150 155 160
90 Leu Leu Trp Gly Ala Asp Ala Glu Lys Lys Gln Gln Cys Ser Phe Lys
91 165 170 175
92 Gly Lys Asp Pro Gln Arg Asp Cys Gln Asn Tyr Ile Lys Ile Leu Leu
93 180 185 190
94 Pro Leu Ser Gly Ser His Leu Phe Thr Cys Gly Thr Ala Ala Phe Ser
95 195 200 205
96 Pro Met Cys Thr Tyr Ile Asn Met Glu Asn Phe Thr Leu Ala Arg Asp
97 210 215 220
98 Glu Lys Gly Asn Val Leu Leu Glu Asp Gly Lys Gly Arg Cys Pro Phe
99 225 230 235 240
100 Asp Pro Asn Phe Lys Ser Thr Ala Leu Val Val Asp Gly Glu Leu Tyr
101 245 250 255
102 Thr Gly Thr Val Ser Ser Phe Gln Gly Asn Asp Pro Ala Ile Ser Arg
103 260 265 270
104 Ser Gln Ser Leu Arg Pro Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu
105 275 280 285
106 Gln Asp Pro Ala Phe Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu Gly

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109 305      310      315      320
110 Gly Gln Glu Phe Glu Phe Phe Glu Asn Thr Ile Val Ser Arg Ile Ala
111      325      330      335
112 Arg Ile Cys Lys Gly Asp Glu Gly Gly Glu Arg Val Leu Gln Gln Arg
113      340      345      350
114 Trp Thr Ser Phe Leu Lys Ala Gln Leu Leu Cys Ser Arg Pro Asp Asp
115      355      360      365
116 Gly Phe Pro Phe Asn Val Leu Gln Asp Val Phe Thr Leu Ser Pro Ser
117      370      375      380
118 Pro Gln Asp Trp Arg Asp Thr Leu Phe Tyr Gly Val Phe Thr Ser Gln
119 385      390      395      400
120 Trp His Arg Gly Thr Thr Glu Gly Ser Ala Val Cys Val Phe Thr Met
121      405      410      415
122 Lys Asp Val Gln Arg Val Phe Ser Gly Leu Tyr Lys Glu Val Asn Arg
123      420      425      430
124 Glu Thr Gln Gln Trp Tyr Thr Val Thr His Pro Val Pro Thr Pro Arg
125      435      440      445
126 Pro Gly Ala Cys Ile Thr Asn Ser Ala Arg Glu Arg Lys Ile Asn Ser
127      450      455      460
128 Ser Leu Gln Leu Pro Asp Arg Val Leu Asn Phe Leu Lys Asp His Phe
129 465      470      475      480
130 Leu Met Asp Gly Gln Val Arg Ser Arg Met Leu Leu Leu Gln Pro Gln
131      485      490      495
132 Ala Arg Tyr Gln Arg Val Ala Val His Arg Val Pro Gly Leu His His
133      500      505      510
134 Thr Tyr Asp Val Leu Phe Leu Gly Thr Gly Asp Gly Arg Leu His Lys
135      515      520      525
136 Ala Val Ser Val Gly Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile
137      530      535      540
138 Phe Ser Ser Gly Gln Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg
139 545      550      555      560
140 Gly Leu Leu Tyr Ala Ala Ser His Ser Gly Val Val Gln Val Pro Met
141      565      570      575
142 Ala Asn Cys Ser Leu Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg
143      580      585      590
144 Asp Pro Tyr Cys Ala Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu
145      595      600      605
146 Tyr Gln Pro Gln Leu Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu Gly
147      610      615      620
148 Ala Ser Ala Lys Asp Leu Cys Ser Ala Ser Ser Val Val Ser Pro Ser
149 625      630      635      640
150 Phe Val Pro Thr Gly Glu Lys Pro Cys Glu Gln Val Gln Phe Gln Pro
151      645      650      655
152 Asn Thr Val Asn Thr Leu Ala Cys Pro Leu Leu Ser Asn Leu Ala Thr
153      660      665      670
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156 His Val Leu Pro Thr Gly Asp Leu Leu Leu Val Gly Thr Gln Gln Leu
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158 Gly Glu Phe Gln Cys Trp Ser Leu Glu Glu Gly Phe Gln Gln Leu Val
159 705                      710                      715                      720
160 Ala Ser Tyr Cys Pro Glu Val Val Glu Asp Gly Val Ala Asp Gln Thr
161                      725                      730                      735
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206 actttggcct gccgcctcct ctccaacctg gcgacccgac tctggctacg caacggggcc 2040

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227 <210> SEQ ID NO: 4

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238 35 40 45
239 Ala Pro Ala Leu Arg Met Leu Arg Thr Ala Met Gly Leu Arg Ser Trp
240 50 55 60
241 Leu Ala Ala Pro Trp Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu
242 65 70 75 80
243 Leu Leu Leu Leu Leu Leu Leu Gln Pro Pro Pro Thr Trp Ala
244 85 90 95
245 Leu Ser Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe
246 100 105 110
247 Leu Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu
248 115 120 125
249 Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu Phe
250 130 135 140
251 Ala Leu Ser Ser Asn Leu Ser Phe Leu Pro Gly Gly Glu Tyr Gln Glu
252 145 150 155 160
253 Leu Leu Trp Gly Ala Asp Ala Glu Lys Lys Gln Gln Cys Ser Phe Lys
254 165 170 175
255 Gly Lys Asp Pro Gln Arg Asp Cys Gln Asn Tyr Ile Lys Ile Leu Leu
256 180 185 190
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VERIFICATION SUMMARY

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date